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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 06 16:59:15 EDT 2007

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Reviewer Comments:

<110> TŠRECI, ™zlem
SAHIN, Ugar
KREITER, Sebastian
Johannes Gutenberg-Universit, t Mainz, vertreten durch den
Pr, sidenten

Please remove all foreign accent marks: they are non-ASCII characters, and cannot be processed.

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

Please try to clarify the above <223> response: can the source of the genetic material be mentioned? This type of response appears in Sequence 8.

<210> 11

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid encoding a fusion protein

The above <223> response needs clarification: what are the sources of the fusion protein? This type of response appears in Sequence 13, too.

Application No: 10575640 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-27 08:37:14.100
Finished: 2007-08-27 08:37:17.698
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 598 ms
Total Warnings: 8
Total Errors: 0
No. of SeqIDs Defined: 66
Actual SeqID Count: 66

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

<210> 1
<211> 78
<212> DNA
<213> Homo sapiens

<400> 1
atgcgggtca cggcgccccg aaccctcatc ctgctgctct cgggagccct ggccctgacc 60
gagacctggg ccggctcc 78

<210> 2
<211> 26
<212> PRT
<213> Homo sapiens

<400> 2

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser
20 25

<210> 3
<211> 168
<212> DNA
<213> Homo sapiens

<400> 3
atcgtgggca ttgttgctgg cctggctgtc ctagcagttg tggtcatcg agctgtggtc 60
gctactgtga tgtgttaggag gaagagctca ggtggaaaag gagggagcta ctctcaggct 120
gcgtccagcg acagtgccta gggctctgat gtgtctctca cagttga 168

<210> 4
<211> 55
<212> PRT
<213> Homo sapiens

<400> 4

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly
35 40 45

Ser Asp Val Ser Leu Thr Ala

50

55

<210> 5

<211> 129

<212> DNA

<213> Homo sapiens

<400> 5

cagagcaaga tgctgagtg 5 agtcgggggc tttgtgctgg gcctgctctt ccttggggcc 60

gggctgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120

ctgagctga 129

<210> 6

<211> 42

<212> PRT

<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu

1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His

20 25 30

Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser

35

40

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

<400> 7

ctgcagggtcg actctagagg atcc 24

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser

1 5

<210> 9

<211> 1683

<212> DNA

<213> Cytomegalovirus

<400> 9

atggagtcgc gcggtcgccg ttgtccgaa atgatatccg tactgggtcc catttcgggg 60

cacgtgctga aagccgtgtt tagtcgcggc gatacgcggg tgctgcccga cgagacgcga 120

ctcctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatcgcag 180

tacacgcccc actcgacgcc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg 240

tactttaacgg gcagcgaggt ggagaacgtg tcggtaacg tgccacaaccc cacgggcccga 300

agcatctgcc ccagccagga gccccatgtcg atctatgtgt acgcgcgtgcc gctcaagatg 360

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cacctgcccc tagctgacgc tggattcac gcgtcgggca agcagatgtg gcaggcgctg 480

ctcacggctc cgggactggc ctggacgcgt cagcagaacc agtggaaaga gcccgcacgtc 540

tactacacgt cagcgttcgt gtttcccacc aaggacgtgg cactgcggca cgtggtgtgc 600

gcgcacgagc tggtttgctc catggagaac acgcgcgcaa ccaagatgca ggtgataggt 660

gaccagtacg tcaagggtgta cctggagtcc ttctgcgagg acgtgcgcctc cggcaagctc 720

tttatgcacg tcacgctggg ctctgacgtg gaagaggacc tgacgatgac ccgcaacccg 780

caacccttca tgcgc(cc)ca cgagcgcaac ggcttacgg tgggtgtcc caaaaatatg 840

ataatcaaac cgggcaagat ctcgcacatc atgctggatg tggctttac ctcacacgag 900

cattttgggc tgcgtgtcc caagagcatc cggggcctga gcatctcagg taacctgttg 960

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cctcagtaca gcgagcaccc cacccatcacc agccagatc gcatccagg caagctttag 1140

taccgacaca cctgggaccg gcacgcacgag ggtgccccc agggcgacga cgacgtctgg 1200

accagcgat cggactccga cgaagaactc gtaaccacgg agcgcaagac gccccgcgtc 1260

accggcgccg ggcgcattggc gggcgccctcc acttccgcgg gcccacaacg caaatcagca 1320

tcctcggcga cggcgtgcac gtcgggcgtt atgacacgcg gcccgcctaa ggccgagtcc 1380

accgtcgcbc ccgaagagga caccgacgag gattccgaca acgaaatcca caatccggcc 1440
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gctacggttc agggtcagaa tctgaagtac caggaattct tctggacgc caacgacatc 1560
taccgcacatct tcgccaatt ggaaggcgta tggcagcccg ctgcgcacc caaacgtcgc 1620
cgccaccggc aagacgcctt gcccgggcca tgcacatcgccct cgacgccc aaagcaccga 1680
ggc 1683

<210> 10
<211> 561
<212> PRT
<213> Cytomegalovirus

<400> 10

Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly
1 5 10 15

Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser
275 280 285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr

370

375

380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys
405 410 415

Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
545 550 555 560

Gly

<210> 11
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleic acid encoding a fusion protein

<400> 11

atgcgggtca	cggcccccg	aaccctcata	ctgctgtct	cgggagccct	ggccctgacc	60
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cgcgttgtc	ccgaaatgat	atccgtactg	ggtcccattt	cggggcacgt	gctgaaagcc	180
gtgttagtc	gcggcgatac	gccgggtctg	ccgcacgaga	cgcgactcct	gcagacgggt	240
atccacgtac	gcgtgagcca	gccctcgctg	atcttggtat	cgcagtacac	gcccgactcg	300
acgccatgcc	accggggcga	caatcagctg	caggtgcagc	acacgtactt	tacgggcagc	360
gaggtggaga	acgtgtcggt	caacgtgcac	aaccccacgg	gccgaagcat	ctgccccagc	420
caggagccca	tgtcgatcta	tgtgtacgct	ctgcccgtca	agatgtgaa	catccccagc	480
atcaacgtgc	accactaccc	gtcgccggcc	gagcgcaaac	accgacacct	gcccgttagct	540
gacgctgtga	ttcacgcgtc	gggcaagcag	atgtggcagg	cgcgtctcac	ggtctcgggta	600
ctggcctgg	cgcgtcagca	gaaccagtgg	aaagagcccg	acgtctacta	cacgtcagcg	660
ttcgtgtttc	ccaccaagga	cgtggactg	cggcacgtgg	tgtgcgcgca	cgagctggtt	720
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aagatctcgc	acatcatgct	ggatgtggct	tttacctcac	acgagcattt	tgggctgctg	1020
tgtcccaaga	gcatccgggg	cctgagcatc	tcaggttaacc	tgttgatgaa	cgggcagcag	1080
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cacccacct	tcaccagcca	gtatcgcatc	cagggcaagc	ttgagtaccg	acacacctgg	1260
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tgcacgtcg	gcgttatgac	acgcggccgc	cttaaggccg	agtccaccgt	cgcgccccaa	1500
gaggacaccc	acgaggattc	cgacaacgaa	atccacaatc	cggccgtgtt	cacctggccg	1560
ccctggcagg	ccggcatcct	ggcccccaac	ctggtgccca	tggtggtac	ggttcagggt	1620

cagaatctga agtaccagga attcttctgg gacgccaacg acatctaccg catttcgcc 1680
gaatttggaaag gcgtatggca gcccgcgtcg caacccaaac gtcgcccggca ccggcaagac 1740
gccttgcggc ggccatgcat cgccctcgacg cccaaaaagc accgaggtgg atccatcgta 1800
ggcattgttg ctggcctggc tgccttagca gttgtggta tcggagctgt ggtcgctact 1860
gtgatgtgta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc 1920
agcgacagtg cccagggctc tgatgtgtct ctcacagctt ga 1962

<210> 12
<211> 653
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<400> 12

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg
20 25 30

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser
35 40 45

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser
260 265 270

Gly Lys Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp
275 280 285

Leu Thr Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg
290 295 300

Asn Gly Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly
305 310 315 320

Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His
325 330 335

Phe Gly Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly
340 345 350

Asn Leu Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile
355 360 365

Arg Glu Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe
370 375 380

Phe Phe Asp Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu
385 390 395 400

His Pro Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr
405 410 415

Arg His Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp
420 425 430

Asp Val Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr
435 440 445

Glu Arg Lys Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala
450 455 460

Ser Thr Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala
465 470 475 480

Cys Thr Ser Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr
485 490 495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys
580 585 590

Lys His Arg Gly Gly Ser Ile Val Gly Ile Val